IN THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1 (Currently Amended): An isolated polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO: 2 ~~from coryneform bacteria, comprising a polynucleotide sequence which codes for the lysR2 gene, chosen from the group consisting of~~

~~a) polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,~~

~~b) polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least to [sic] 70% to the amino acid sequence of SEQ ID No. 2,~~

~~c) polynucleotide which is complementary to the polynucleotides of a) or b), and~~

~~d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b), or c),~~

~~the polypeptide preferably having the activity of the transcription regulator LysR2~~.

Claim 2 (Currently Amended): ~~A~~ The polynucleotide ~~as claimed in~~ of claim 1, wherein ~~the~~ said polynucleotide is ~~a preferably recombinant~~ DNA ~~which is capable of replication in coryneform bacteria~~.

Claim 3 (Currently Amended): ~~A~~ The polynucleotide ~~as claimed in~~ of claim 1, wherein ~~the~~ said polynucleotide is an RNA.

Claim 4 (Currently Amended): ~~A DNA as claimed in claim 2 which is capable of replication~~ An isolated polynucleotide, comprising

(i) ~~the~~ a nucleotide sequence shown in SEQ ID No. 1, or

(ii) a full complement of a nucleotide sequence shown in SEQ I NO: 1~~at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or~~

~~(iii) at least one sequence which hybridizes with the sequences complementary to sequences (i) or (ii), and optionally~~

~~(iv) (iv)[sic] sense mutations of neutral function in (i) which do not modify the activity of the protein/polypeptide~~.

Claim 5 (Currently Amended): ~~A~~ An isolated polynucleotide, comprising a nucleic acid sequence of nucleotides 232 to 1161 of ~~as claimed in claim 2, comprising the nucleic acid sequence as shown in~~ SEQ ID No. 1.

Claim 6 (Currently Amended): ~~The~~ A vector pCR2.1lysR2int, ~~which~~

~~6.1 carries an internal fragment of the citA gene 439 by in size,~~

~~6.2 the restriction map of which is reproduced in figure 1, and~~

~~6.3~~ which is deposited in the E.coli strain TOPlOF/pCR2.1lysR2int under no. DSM 13617 ~~at the Deutsche Sammlung fur Mikroorganismen and Zellenkulturen [German Collection of Microorganisms and Cell Cultures]~~.

Claim 7 (Currently Amended): A recombinant coryneform bacterium ~~in which the lysR2 gene is attenuated, preferably eliminated, in particular by deletion~~ lacking a polypeptide having an amino acid sequence of SEQ ID NO: 2, wherein said lacking is

achieved by one or more methods of mutagenesis of the polynucleotide encoding the polypeptide having the amino acid sequence of SEQ ID NO: 2 selected from the group consisting of deletion mutagenesis of two or more codons, insertion or deletion mutagenesis of at least one nucleotide and transition or transversion mutagenesis of at least one nucleotide with incorporation of a nonsense mutation.

Claim 8 (Currently Amended): A process for the preparation of L-amino acids, ~~in particular L-lysine and L-valine,~~ which comprises ~~carrying out~~ the following steps,

a) ~~fermentation of~~ fermenting cells comprising the bacteria of Claim 7 ~~which produce the desired L-amino acid and in which at least the lysR2 gene is attenuated~~,

b) ~~concentration~~ concentrating said L-amino acids in a medium or in the cells of the bacteria; and

c) ~~isolation of~~ isolating said ~~the~~ L-amino ~~acid~~ acids.

Claim 9 (Currently Amended): ~~A~~ The process ~~as claimed in~~ of claim 8, wherein bacteria in which further genes of the biosynthesis pathway of ~~the desired~~ L-amino ~~acid~~ acids are additionally enhanced are employed.

Claim 10-12 (Canceled):

Claim 13 (Currently Amended): ~~A~~ The process ~~as claimed in~~ of claim 8, wherein ~~for the preparation of~~ said L-amino acids~~, in particular~~ are L-lysine~~,~~ and wherein said bacteria further comprise at least on gene whose expression is enhanced, wherein said gene is ~~in which at the same time one or more of the genes chosen~~ selected from the group consisting of

~~13.1~~ the dapA gene which codes for dihydrodipicolinate synthase,

~~13.2~~ the eno gene which codes for enolase,

~~13.3~~ the zwf gene which codes for the zwf gene product,

~~13.4~~ the pyc gene which codes for pyruvate carboxylase,

~~13.5~~ the lysE gene which codes for lysine export, and

~~13.6~~ the lysC gene which codes for a feed-back resistant aspartate kinase

~~13.7 the zwal gene which codes for the Zwal protein is or are enhanced, preferably over-expressed, are fermented~~.

Claim 14 (Currently Amended): ~~A~~ The process ~~as claim in~~ of claim 8, wherein

~~At the same time one or more of the genes chosen from the group consisting of:~~ said bacteria further comprises at least one gene whose expression is attenuated, wherein said gene is selected from the group consisting of

~~14.1~~ the pck gene which codes for phosphoenol pyruvate carboxykinase,

~~14.2~~ the pgi gene which codes for glucose 6-phosphate isomerase,

~~14.3~~ the poxB gene which codes for pyruvate oxidase,

~~14.4 the zwa2 gene which codes for the Zwa2 protein,~~

~~14.5~~ the hom gene which codes for homoserine dehydrogenase

~~14.6~~ the thrB gene which codes for homoserine kinase, and

~~14.7~~ the panD gene which codes for aspartate decarboxylase

~~is or are attenuated, in particular eliminated~~.

Claim 15 (Currently Amended): A process as claimed in claim 8,

wherein said L-amino acids are L-valine and wherein said bacteria further comprises at least one gene whose expression is enhanced, wherein said gene is selected from the group consisting of

~~for the preparation of L-amino acids, in particular L-valine, bacteria in which at the same time one or more of the genes chosen from the group consisting of~~

~~15.1~~ the ilvBN gene which codes for acetohydroxy-acid synthase,

~~15.2~~ the ilvD gene which codes for dihydroxy-acid dehydratase, and

~~15.3~~ the mqo gene which codes for malate:quinone oxidoreductase

~~is or are enhanced, in particular over-expressed, are fermented~~.

Claim 16 (Currently Amended): ~~A process as claimed in one or more of the preceding claims,~~ The bacterium of Claim 7,

wherein said bacterium

~~microorganisms of~~ are the species Corynebacterium glutamicum or Brevibacterium lactofermentum ~~are employed~~.

Claim 17 (Withdrawn): A process for discovering RNA, cDNA and DNA in order to isolate nucleic acids, or polynucleotides or genes which code for the transcription regulator LysR2 or have a high similarity with the sequence of the lysR2 gene,

which comprises

employing the polynucleotide sequences as claimed in claims 1 to 4 as hybridization probes.

Claim 18 (Withdrawn): A process as claimed in claim 15,

wherein arrays, micro arrays or DNA chips are employed.

Claim 19 (New) The process of Claims 8, wherein said L-amino acids are L-lysine, L-valine or mixtures thereof.

Claim 20 (New) An isolated polynucletide consisting of a fragment of at least 15 consecutive nucleotides of SEQ NO: 1 or a full complement thereof.

Claim 21 (New) The polynucleotide of Claim 20, wherein said polynucleotide is a probe or a primer.

Claim 22 (New) An isolated polynucleotide, comprising a polynucleotide sequence that encodes a polypeptide having an amino acid sequence that is at least 90% identical to SEQ ID NO: 2 wherein said polypeptide has transcription regulator LysR2 activity.

Claim 23 (New) The isolated polynucleotide according to Claim 23, wherein said polynucleotide encodes a polypeptide having an amino acid sequence that is at least 95% identical to SEQ ID NO: 2.

Claim 24 (New) The isolated polynucleotide according to Claim 23, wherein said polynucleotide encodes a polypeptide having an amino acid sequence that is at least 97% identical to SEQ ID NO: 2.

Claim 25 (New) The isolated polynucleotide according to Claim 23, wherein said polynucleotide encodes a polypeptide having an amino acid sequence that is at least 99% identical to SEQ ID NO: 2.